



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/600,862A

DATE: 09/13/2004
TIME: 09:42:32

Input Set : A:\39383.txt
Output Set: N:\CRF4\09132004\J600862A.raw

3 <110> APPLICANT: Zankel et al.
5 <120> TITLE OF INVENTION: USE OF THE CHAPERONE RECEPTOR-ASSOCIATED PROTEIN (RAP) FOR
THE

6 DELIVERY OF THERAPEUTIC COMPOUNDS TO THE BRAIN AND OTHER TISSUES

8 <130> FILE REFERENCE: 30610/39383

10 <140> CURRENT APPLICATION NUMBER: US 10/600,862A

11 <141> CURRENT FILING DATE: 2003-06-20

13 <160> NUMBER OF SEQ ID NOS: 28

15 <170> SOFTWARE: PatentIn version 3.2

17 <210> SEQ ID NO: 1

18 <211> LENGTH: 323

19 <212> TYPE: PRT

20 <213> ORGANISM: Homo sapiens

22 <400> SEQUENCE: 1

24 Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro Lys Arg Glu Ser

25 1 5 10 15

28 Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu Trp Glu Lys Ala

29 20 25 30

32 Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu Leu His Ala Asp

33 35 40 45

36 Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys Lys Leu Lys Leu

37 50 55 60

40 Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg Leu Ile Arg Asn

41 65 70 75 80

44 Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly Lys Lys Asp Ala

45 85 90 95

48 Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln Glu Asp Gly Leu

49 100 105 110

52 Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr Ser Gly

53 115 120 125

56 Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe Leu His

57 130 135 140

60 His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr Leu Ser

61 145 150 155 160

64 Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp Leu Ser

65 165 170 175

68 Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu Lys Glu

69 180 185 190

72 Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg Val Ser

73 195 200 205

76 His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg Val Ile

77 210 215 220

80 Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys Glu Leu

81 225 230 235 240

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84 Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile Glu Lys
 85 245 250 255
 88 His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys Leu Arg
 89 260 265 270
 92 His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser Arg Glu
 93 275 280 285
 96 Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr Thr Val
 97 290 295 300
 100 Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser Arg Ala Arg His
 101 305 310 315 320
 103 Asn Glu Leu
 106 <210> SEQ ID NO: 2
 107 <211> LENGTH: 209
 108 <212> TYPE: PRT
 109 <213> ORGANISM: Homo sapiens
 111 <400> SEQUENCE: 2
 113 Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr Ser Gly Lys Phe
 114 1 5 10 15
 117 Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe Leu His His Lys
 118 20 25 30
 121 Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr Leu Ser Arg Thr
 122 35 40 45
 125 Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp Leu Ser Asp Ile
 126 50 55 60
 129 Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu Lys Glu Lys Leu
 130 65 70 75 80
 133 Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg Val Ser His Gln
 134 85 90 95
 137 Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg Val Ile Asp Leu
 138 100 105 110
 141 Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys Glu Leu Glu Ala
 142 115 120 125
 145 Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile Glu Lys His Asn
 146 130 135 140
 149 His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys Leu Arg His Ala
 150 145 150 155 160
 153 Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser Arg Glu Lys His
 154 165 170 175
 157 Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr Thr Val Lys Lys
 158 180 185 190
 161 His Leu Gln Asp Leu Ser Gly Arg Ile Ser Arg Ala Arg His Asn Glu
 162 195 200 205
 165 Leu
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 170 <211> LENGTH: 33
 171 <212> TYPE: DNA
 172 <213> ORGANISM: Artificial sequence
 174 <220> FEATURE:
 175 <223> OTHER INFORMATION: Synthetic primer

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177 <400> SEQUENCE: 3
 178 ccgcgtggat ccccccaggct ggaaaaagctg tgg 33
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 182 <211> LENGTH: 35
 183 <212> TYPE: DNA
 184 <213> ORGANISM: Artificial sequence
 186 <220> FEATURE:
 187 <223> OTHER INFORMATION: Synthetic primer
 189 <400> SEQUENCE: 4
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 193 <210> SEQ ID NO: 5
 194 <211> LENGTH: 205
 195 <212> TYPE: PRT
 196 <213> ORGANISM: Homo sapiens
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 201 1 5 10 15
 204 Val Arg Leu Thr Ser Cys Ala Arg Val Leu His Tyr Lys Glu Lys Ile
 205 20 25 30
 208 His Glu Tyr Asn Val Leu Leu Asp Thr Leu Ser Arg Ala Glu Glu Gly
 209 35 40 45
 212 Tyr Glu Asn Leu Leu Ser Pro Ser Asp Met Thr His Ile Lys Ser Asp
 213 50 55 60
 216 Thr Leu Ala Ser Lys His Ser Glu Leu Lys Asp Arg Leu Arg Ser Ile
 217 65 70 75 80
 220 Asn Gln Gly Leu Asp Arg Leu Arg Lys Val Ser His Gln Leu Arg Pro
 221 85 90 95
 224 Ala Thr Glu Phe Glu Glu Pro Arg Val Ile Asp Leu Trp Asp Leu Ala
 225 100 105 110
 228 Gln Ser Ala Asn Phe Thr Glu Lys Glu Leu Glu Ser Phe Arg Glu Glu
 229 115 120 125
 232 Leu Lys His Phe Glu Ala Lys Ile Glu Lys His Asn His Tyr Gln Lys
 233 130 135 140
 236 Gln Leu Glu Ile Ser His Gln Lys Leu Lys His Val Glu Ser Ile Gly
 237 145 150 155 160
 240 Asp Pro Glu His Ile Ser Arg Asn Lys Glu Lys Tyr Val Leu Leu Glu
 241 165 170 175
 244 Glu Lys Thr Lys Glu Leu Gly Tyr Lys Val Lys Lys His Leu Gln Asp
 245 180 185 190
 248 Leu Ser Ser Arg Val Ser Arg Ala Arg His Asn Glu Leu
 249 195 200 205
 252 <210> SEQ ID NO: 6
 253 <211> LENGTH: 3702
 254 <212> TYPE: DNA
 255 <213> ORGANISM: Artificial sequence
 257 <220> FEATURE:
 258 <223> OTHER INFORMATION: RAP-GAA fusion sequence
 260 <400> SEQUENCE: 6
 261 cttaccggcca tgcggggtcc gagcggggct ctgtggctgc tcctggctct ggcaccgtg 60

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263	ctcgatcct	actcgccgg	gaagaaccag	cccaagccgt	ccccgaaacg	cgagtccgga	120
265	gaggagtcc	gcatggagaa	gttgaaccag	ctgtgggaga	aggcccacg	actgcacatct	180
267	cctccgtga	ggctggccg	gctccacgct	gatctgaaga	tacaggagag	ggacgaactc	240
269	gccttggaga	aactaaagct	tgacgggtt	gacgaagatg	gggagaagga	agcgagactc	300
271	atacgcaacc	tcaatgtcat	cttggccaag	tatggtctgg	acggaaagaa	ggacgctcg	360
273	caggtgacca	gcaactccct	cagtggacc	cagaagacg	ggctggatga	ccccaggctg	420
275	gaaaagctgt	ggcacaaggc	gaagacctt	ggaaaattct	ccggcgaaga	actggacaag	480
277	ctctggcg	agttcctgca	tcacaaagag	aaagttcacg	agtacaacgt	cctgctggag	540
279	accctgagca	ggaccgaaga	aatccacgag	aacgtcatta	gcccctcg	cctgagcgcac	600
281	atcaaggggca	gcgtcctgca	cagcaggac	acggagctg	aggagaagct	gcmcagcatc	660
283	aaccaggggc	tggaccgcct	gcccgggtc	agccaccagg	gctacagcac	tgaggctgag	720
285	ttcgaggagc	ccagggtgtat	tgacctgtgg	gacctggcgc	agtccggcaa	cctcacggac	780
287	aaggagctgg	aggcgttccg	ggaggagctc	aagcacttcg	aagccaaat	cgagaagcac	840
289	aaccactacc	agaagcagct	ggagattgcg	cacgagaagc	tgaggcacgc	agagagctg	900
291	ggcgacggcg	agcgtgtgag	ccgcagccgc	gagaagcacg	ccctgttga	ggggcggacc	960
293	aaggagctgg	gctacacggt	gaagaagcat	ctgcaggacc	tgtccggcag	gatctccaga	1020
295	gctcgccgcg	aggcagaaac	cggtgcacac	ccccggcg	ccagaggcgt	gcccacacag	1080
297	tgcgacgtcc	cccccaacag	ccgcttgcgt	tgcgtccctg	acaaggccat	cacccaggaa	1140
299	cagtgcgagg	cccgccggct	ctgtacatc	cctgcaaaagc	aggggctgca	gggagcccag	1200
301	atggggcagc	cctgggtgtt	cttcccaccc	agtacccca	gctacaagct	ggagaacctg	1260
303	agtcctctg	aaatgggcta	cacggccacc	ctgaccctgta	ccaccccccac	cttcttcccc	1320
305	aaggacatcc	tgaccctgca	gctggacgtg	atgatggaga	ctgagaaccg	cctccacttc	1380
307	acgatcaaag	atccagctaa	caggcgtac	gaggtgcct	tggagacccc	gegtgtccac	1440
309	agccgggcac	cgtccccact	ctacagcgt	gagttctccg	aggagccctt	cgggggtgatc	1500
311	gtgcaccggc	agctggacgg	ccgcgtgtg	ctgaacacga	cggtggcgcc	cctgttcttt	1560
313	gcccggccgt	tccttgcgt	gtccacctcg	ctgcctctcg	agtataatc	aggcctcgcc	1620
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319	gaggacggcg	ggtccggcaca	cggggtgttc	ctgtaaaca	gcaatgccat	ggatgtggtc	1800
321	ctgcagccg	gccctgcct	tagctggagg	tcgacagg	ggatccttga	tgtctacatc	1860
323	tccctggccc	cagacccaa	gagcgtgt	cagcgttacc	tggacgtt	ggatcacccg	1920
325	tcatgcgc	catactgggg	cctgggtt	cacctgtg	gctgggct	ctccctccacc	1980
327	gtatcaccc	gccaggtgt	ggagaacat	accaggccc	acttccccc	ggacgtccaa	2040
329	ttggaaacgacc	tggactacat	ggactcccg	aggacttca	cgttcaacaa	ggatggcttc	2100
331	cgggacttcc	cgccatgg	cgaggagct	caccaggcg	gcccgcgct	catgtatgtc	2160
333	gtggatctg	ccatcagcag	ctcggccct	gcccggagct	acaggcccta	cgacgagggt	2220
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337	cccggttca	ctgccttccc	cgacttacc	aacccacag	ccctggct	gtgggaggac	2340
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341	ctttcaact	tcatcagagg	ctctgaggac	ggctgcccc	acaatgag	ggagaaccca	2460
343	ccctacgtc	ctgggttgt	tggggggacc	ctccaggccg	ccaccatct	tgccctccagc	2520
345	caccagttt	tctccacaca	ctacaacctg	cacaacctt	acggcctg	cgaagccatc	2580
347	gcctcccaca	gggcgttgt	gaaggctcg	ggcacacgc	catttgcgt	ctcccgctcg	2640
349	acctttgt	gccacggccg	atacggccgc	cactggacgg	gggacgtgt	gagtcctgg	2700
351	gagcagctcg	cctccctcg	gccagaaatc	ctgcagttt	acctgctgg	gggtgcctctg	2760
353	gtcggggccg	acgtctgcgg	cttccctggc	aacacctcg	aggagctgt	tgtgcgttgg	2820
355	acccagctgg	gggccttcta	ccccttcatg	cggaaccaca	acagcctgt	cagtctgccc	2880
357	caggagccgt	acagttcag	cgagccggcc	cagcaggcc	tgaggaaggc	cctcaccctg	2940
359	cgctacgcac	tcctcccca	cctctacaca	ctgttccacc	aggcccacgt	cgcgggggag	3000

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361	accgtggccc	ggcccttctt	cctggagttc	cccaaggact	ctagcacctg	gactgtggac	3060
363	caccagctcc	tgtgggggga	ggccctgctc	atcacccag	tgctccaggc	cgggaggcc	3120
365	gaagtgaactg	gctacttccc	cttgggcaca	tggtagcacc	tgcagacgg	gcataatagag	3180
367	gcccttggca	gcctccacc	cccacctgca	gctccccgtg	agccagccat	ccacagcgag	3240
369	gggcagtggg	tgacgctgcc	ggcccccctg	gacaccatca	acgtccacct	ccgggctggg	3300
371	tacatcatcc	ccctgcaggg	ccctggcctc	acaaccacag	agtcccggca	gcagcccatg	3360
373	gccctggctg	tggccctaac	caagggttga	gaggccccgag	gggagctgtt	ctgggacgat	3420
375	ggagagagcc	tggaagtgt	ggagcgaggg	gcctacacac	aggtcatctt	cctggccagg	3480
377	aataacacga	tcgtgaatga	gctggtaacgt	gtgaccagtg	agggagctgg	cctgcagctg	3540
379	cagaagggtga	ctgtcctggg	cgtggccacg	gcccggcagc	aggtcccttc	caacgggtg	3600
381	cctgtctcca	acttcaccta	cagcccccac	accaagggtcc	tggacatctg	tgtctcgctg	3660
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388	<212> TYPE: PRT						
389	<213> ORGANISM: Artificial sequence						
391	<220> FEATURE:						
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401	20	25	30				
404	Lys Arg Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu						
405	35	40	45				
408	Trp Glu Lys Ala Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu						
409	50	55	60				
412	Leu His Ala Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys						
413	65	70	75	80			
416	Lys Leu Lys Leu Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg						
417	85	90	95				
420	Leu Ile Arg Asn Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly						
421	100	105	110				
424	Lys Lys Asp Ala Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln						
425	115	120	125				
428	Glu Asp Gly Leu Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala						
429	130	135	140				
432	Lys Thr Ser Gly Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg						
433	145	150	155	160			
436	Glu Phe Leu His His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu						
437	165	170	175				
440	Glu Thr Leu Ser Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro						
441	180	185	190				
444	Ser Asp Leu Ser Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr						
445	195	200	205				
448	Glu Leu Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu						
449	210	215	220				
452	Arg Arg Val Ser His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu						
453	225	230	235	240			

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